



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gregory Plowman
Bahija Jallal

(ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
PTP RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/095,478
(B) FILING DATE: June 10, 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049,756
(B) FILING DATE: June 11, 1997

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1785 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

B₂

GGTTATGTCT	GACTCACTGC	ACTGGAGTTT	GGCAAAAGCA	TCTCAGAAGT	GGTTGTGCTT	60
TTTTGAATGA	AATGATCAAT	GGAGTGCTCC	AGTTGTATGC	TGGCCTCTGG	ATACTAACTA	120
GACCTGCCTG	ACTCCAGGAA	CTAAGGCTCA	GTATCTGCAG	AAGCTTTTTG	CCCATCTCAT	180
TCCGGCTATG	GGGACAACAT	GTCTTCACCC	AGGAAGGTTA	GAGGAAAAAC	TGGAAGAGAT	240
AATGATGAAG	AGGAGGGTAA	TTCAGGTAAC	CTGAATCTCC	GCAACTCTTT	GCCTTCATCG	300
AGTCAGAAAA	TGACGCCTAC	GAAGCCGATT	TTTGGGAATA	AAATGAATTC	AGAGAATGTA	360
AAACCCTCCC	ATCACCTGTC	ATTCTCAGAT	AAGTATGAGC	TTGTTTACCC	AGAGCCTTTG	420
GAAAGTGACA	CTGATGAGAC	TGTGTGGGAT	GTCACTGACC	GGTCTCTCAG	AAACAGGTGG	480
AACAGTATGG	ATTCAGAGAC	TGCAGGGCCG	TCAAAGACTG	TCTCCCCAGT	GCTTTCTGGT	540
AGTAGTAGGC	TGTCAAAGGA	CAGTGAACA	TCTGTCTCTG	AAAAGGAGCT	AACTCAGTTG	600
GCTCAGATTG	GACCATTAAT	ATTCAACAGT	TCTGCACGGT	CTGCTATGCG	GGATTGTTTG	660
AACACGCTTC	AGAAAAAAGA	AGAACTTGAT	ATCATCCGTG	AGTTTTTGGG	GTTAGAACAA	720
ATGACTCTGC	CTGATGACTT	CAATTCTGGG	AATACACTAC	AGAACAGAGA	TAAGAACAGA	780
TACCGAGATA	TTCTTCCATA	TGATTCAACA	CGTGTTCCTC	TTGGAAAAAA	CAAGGACTAC	840
ATCAACGCTA	GTTATATTAG	AATAGTAAAT	CATGAAGAAG	AGTATTTTTA	TATTGCCACT	900
CAAGGACCAT	TGCCAGAAAC	TATAGAAGAC	TTTTGGCAAA	TGGTTCTGGA	AAATAATTGT	960
AATGTTATTG	CTATGATAAC	CAGAGAGATA	GAATGTGGAG	TTATCAAGTG	TTACAGTTAC	1020
TGGCCCATTT	CTCTGAAGGA	GCCTTTGGAA	TTCAACACT	TTAGTGTCTT	TCTGGAGACC	1080
TTTCATGTAA	CTCAATATTT	CACCGTTCGA	GTATTTTCTG	TTGTGAAGAA	GTCCACAGGA	1140
AAGAGCCAAT	GTGTAAAACA	CTTGCAGTTC	ACCAAGTGGC	CAGACCATGG	CACTCCTGCC	1200
TCAGCAGATT	TTTTCATAAA	ATATGTCCGT	TATGTGAGGA	AGAGCCACAT	TACAGGACCC	1260
CTCCTTGTTT	ACTGCAGTGC	TGGTGTAGGC	CGAACAGGGG	TGTTTCATATG	TGTGGATGTT	1320
GTGTTCTCTG	CCATCGAGAA	GAAGTACTCT	TTTGACATTA	TGAACATAGT	GACCCAGATG	1380
AGAAAGCAGC	GCTGTGGCAT	GATTCAAACC	AAGGAGCAGT	ACCAGTTTTG	TTATGAAATT	1440
GTGCTTGAAG	TTCTTCAGAA	CCTTCTGGCT	TTGTATTAA	AGAGACTTCT	GCGCCTGTCC	1500
CTCGAGGTTA	CCGAGCAGCT	TGGAGCCTGA	GCCGTGCTGA	AGCGTCTGCG	GGCCGTGCAG	1560
TCTGCCTTCT	GATTTTTTCTC	TCTGAAAGTC	CCTGAAGGTA	GCACTACTGG	GCACAGAGTG	1620
AACTGTTTCC	ACTTGATCTT	TCTGAAACA	AGCAAAATAC	CCTCCATGCC	TTCTACGGAA	1680
ACGGAAGTTG	CATGAAACAA	CCTCCGCTTG	GCTGTCTGGT	TTGTGGTATT	ACAGAGCTTA	1740
ATAAAAGACT	TAGATGTGAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA		1785

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1896 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTTGTGCTT 60

TTTTGAATGA AATGATCAAT GGAGTGCTCC AGTTGTATGC TGGCCTCTGG ATACTAACTA 120
 GACCTGCCTG ACTCCAGGAA CTAAGGCTCA GTATCTGCAG AAGCTTTTTG CCCATCTCAT 180
 TCCGGCTATG GGGACAACAT GTCTTCACCC AGGAAGGTTA GAGGAAAAAC TGGAAGAGAT 240
 AATGATGAAG AGGAGGGTAA TTCAGGTAAC CTGAATCTCC GCAACTCTTT GCCTTCATCG 300
 AGTCAGAAAA TGACGCCTAC GAAGCCGGTA CAAAATAAAA ATCTCATGAA GTATGAAGAA 360
 CACTTAGATA TATTGATGGT GTTTTTATTG ATAAAAACCA TATGGTATAA TGTCTTCAAA 420
 TTATGGAAAG GCAAGCTTAT TTTTGGGAAT AAAATGAATT CAGAGAATGT AAAACCCTCC 480
 CATCACCTGT CATTCTCAGA TAAGTATGAG CTTGTTTACC CAGAGCCTTT GGAAAGTGAC 540
 ACTGATGAGA CTGTGTGGGA TGTCAGTGAC CGGTCTCTCA GAAACAGGTG GAACAGTATG 600
 GATTCAGAGA CTGCAGGGCC GTCAAAGACT GTCTCCCCAG TGCTTTCTGG TAGTAGTAGG 660
 CTCTCAAAGG ACACTGAAAC ATCTGTCTCT GAAAAGGAGC TAACTCAGTT GGCTCAGATT 720
 CGACCATTAA TATTCAACAG TTCTGCACGG TCTGCTATGC GGGATTGTTT GAACACGCTT 780
 CAGAAAAAAG AAGAACTTGA TATCATCCGT GAGTTTTTGG AGTTAGAACA AATGACTCTG 840
 CCTGATGACT TCAATTCTGG GAATACACTA CAGAACAGAG ATAAGAACAG ATACCGAGAT 900
 ATTCTTCCAT ATGATTCAAC ACGTGTTTCT CTTGGAAAAA ACAAGGACTA CATCAACGCT 960
 AGTTATATTA GAATAGTAAA TCATGAAGAA GAGTATTTTT ATATTGCCAC TCAAGGACCA 1020
 TTGCCAGAAA CTATAGAAGA CTTTTGGCAA ATGGTCTTGG AAAATAATTG TAATGTTATT 1080
 GCTATGATAA CCAGAGAGAT AGAATGTGGA GTTATCAAGT GTTACAGTTA CTGGCCCATT 1140
 TCTCTGAAGG AGCCTTTGGA ATTCGAACAC TTTAGTGTCT TTCTGGAGAC CTTTCATGTA 1200
 ACTCAATATT TCACCGTTCT AGTATTTTCT ATTGTGAAGA AGTCCACAGG AAAGAGCCAA 1260
 TGTGTAAAAC ACTTGCAAGT CACCAAGTGG CCAGACCATG GCACTCCTGC CTCAGCAGAT 1320
 TTTTTCATAA AATATGTCCG TTATGTGAGG AAGAGCCACA TTACAGGACC CCTCCTTGTT 1380
 CACTGCAGTG CTGGTGTAGG CCGAACAGGG GTGTTTCATAT GTGTGGATGT TGTGTTCTCT 1440
 GCCATCGAGA AGAACTACTC TTTTGACATT ATGAACATAG TGACCCAGAT GAGAAAGCAG 1500
 CGCTGTGGCA TGATTCAAAC CAAGGAGCAG TACCAGTTTT GTTATGAAAT TGTGCTTGAA 1560
 GTTCTTCAGA ACCTTCTGGC TTTGTATTAA GAGAGACTTC TGCGCCTGTC CCTCGAGGTT 1620
 ACCGAGCAGC TTGGAGCCTG AGCCGTGCTG AAGCGTCTGC GGGCCGTGCA GTCTGCCTTC 1680
 TGATTTTTCT CTCTGAAAGT CCCTGAAGGT AGCACTACTG GGCACAGAGT GAACTGTTTC 1740
 CACTTGATCT TTCTGAAACA GAGCAAAATA CCCTCCATGC CTTCTACGGA AACGGAAGTT 1800
 GCATGAAACA ACCTCCGCTT GGCTGTCTGG TTTGTGGTAT TACAGAGCTT AATAAAAGAC 1860
 TTAGATGTGA AAAAAAAAAA AAAAAAAAAA AAAAAA 1896

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTTGTGCTT 60

TTTTGAATGA AATGATCAAT GGAGTGCTCC AGTTGTATGC TGGCCTCTGG ATACTAACTA 120
 GACCTGCCTG ACTCCAGGAA CTAAGGCTCA GTATCTGCAG AAGCTTTTTG CCCATCTCAT 180
 TCCGGCTATG GGGACAACAT GTCTTCACCC AGGAAGGTTA GAGGAAAAAC TGGAAGAGAT 240
 AATGATGAAG AGGAGGGTAA TTCAGGTAAC CTGAATCTCC GCAACTCTTT GCCTTCATCG 300
 AGTCAGAAAA TGACGCCTAC GAAGCCGATT TTTGGGAATA AAATGAATTC AGAGAATGTA 360
 AAACCTCTCC ATCACCTGTC ATTCTCAGAT AAGTATGAGC TTGTTTACCC AGAGCCTTTG 420
 GAAAGTGACA CTGATGAGAC TGTGTGGGAT GTCAGTGACC GGTCTCTCAG AAACAGGTGG 480
 AACAGTATGG ATTCAGAGAC TGCAGGGCCG TCAAAGACTG TCTCCCCAGT GCTTTCTGGT 540
 AGTAGTAGGC TCTCAAAGGA CACTGAAACA TCTGTCTCTG AAAAGGAGCT AACTCAGTTG 600
 GCTCAGATTG GACCATTAAT ATTCAACAGT TCTGCACGGT CTGCTATGCG GGATTGTTTG 660
 AACACGCTTC AGAAAAAAGA AGAAGCTTGAT ATCATCCGTG AGTTTTTGGA GTTAGAACAA 720
 ATGACTCTGC CTGATGACTT CAATTCTGGG AATACACTAC AGAACAGAGA TAAGAACAGA 780
 TACCGAGATA TTCTTCCATA TGATTCAACA CGTGTTCCTC TTGGAAAAAA CAAGGACTAC 840
 ATCAACGCTA GTTATATTAG AATAGTAAAT CATGAAGAAG AGTATTTTTA TATTGCCACT 900
 CAAGGACCAT TGCCAGAAAC TATAGAAGAC TTTTGGCAA TGGTTCTGGA AAATAATTGT 960
 AATGTTATTG CTATGATAAC CAGAGAGATA GAATGTGGAG TTATCAAGTG TTACAGTTAC 1020

TGGCCCATTT CTCTGAAGGA GCCTTTGGAA TTCGAACACT TTAGTGTCTT TCTGGAGACC 1080
 TTTTCATGTAA CTCAATATTT CACCGTTCGA GTATTTTCTG TGTGAAGAA GTCCACAGGA 1140
 AAGAGCCAAT GTGTAAAACA CTTGCAGTTC ACCAAGTGGC CAGACCATGG CACTCCTGCC 1200
 TCAGCAGATT TTTTCATAAA ATATGTCCGT TATGTGAGGA AGAGCCACAT TACAGGACCC 1260
 CTCCTTGTTT ACTGCAGTGC TGGTGTAGGC CGAACAGGGG TGTTTCATATG TGTGGATGTT 1320
 GTGTTCTCTG CCATCGAGAA GAACTACTCT TTTGACATTA TGAACATAGT GACCCAGATG 1380
 AGAAAGCAGC GCTGTGGCAT GATTCAAACC AAGGTTACCG AGCAGCTTGG AGCCTGAGCC 1440
 GTGCTGAAGC GTCTGCGGGC CGTGCAGTCT GCCTTCTGAT TTTTCTCTCT GAAAGTCCCT 1500
 GAAGGTAGCA CTAAGGGGCA CAGAGTGAAC TGTTTCCACT TGATCTTTCT GAACAAGAGC 1560
 AAAATACCCT CCATGCCTTC TACGGAAACG GAAGTTGCAT GAAACAACCT CCGCTTGGCT 1620
 GTCTGGTTTG TGGTATTACA GAGCTTAATA AAAGACTTAG ATGTGAAAAA AAAAAAAAAA 1680
 AAAAAAAAAA AA 1692

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAAATAATT GTAATGTTAT TGCTATGATA ACCAGAGAGA TAGAAGGTGG AGTTATCAAG 60
 TGTTGCAGTT ACTGGCCCGT TTCTCTGAAG GAGCCTTTGG AATTCAAACA CTTTCATGTC 120
 CTTCTGGAGA ACTTTCAGAT AACTCAGTAT TTTGTCATCC GAATATTTCA AATTGTGAAG 180
 AAGTCCACAG GAAAGAGTCA CTCTGTAAAA CACTTGCAGT TCATCAAATG GCCAGACCAT 240
 GGCACCTCTG CCTCAGTAGA TTTTTCATC AAATATGTCC GTTATGTGAG GAAGAGCCAC 300
 ATTACAGGAC CCCTCCTTGT 320

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15
 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30
 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys
 35 40 45
 Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp
 50 55 60
 Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu
 65 70 75 80
 Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95
 Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110
 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu
 115 120 125
 Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140
 Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160
 Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175
 Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190
 Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205
 Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220
 His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240
 Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255
 Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr

260 265 270
 Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285
 Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300
 Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320
 His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335
 Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350
 Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365
 Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380
 Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400
 Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys Tyr Glu Ile Val Leu
 405 410 415
 Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
 420 425

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15
 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30
 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Val Gln Asn Lys Asn
 35 40 45
 Leu Met Lys Tyr Glu Glu His Leu Asp Ile Leu Met Val Phe Leu Leu

50	55	60
Ile Lys Thr Ile Trp Tyr Asn Val Phe Lys Leu Trp Lys Gly Lys Leu 65 70 75 80		
Ile Phe Gly Asn Lys Met Asn Ser Glu Asn Val Lys Pro Ser His His 85 90 95		
Leu Ser Phe Ser Asp Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu 100 105 110		
Ser Asp Thr Asp Glu Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg 115 120 125		
Asn Arg Trp Asn Ser Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr 130 135 140		
Val Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu 145 150 155 160		
Thr Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro 165 170 175		
Leu Ile Phe Asn Ser Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn 180 185 190		
Thr Leu Gln Lys Lys Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu 195 200 205		
Leu Glu Gln Met Thr Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu 210 215 220		
Gln Asn Arg Asp Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser 225 230 235 240		
Thr Arg Val Pro Leu Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr 245 250 255		
Ile Arg Ile Val Asn His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln 260 265 270		
Gly Pro Leu Pro Glu Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu 275 280 285		
Asn Asn Cys Asn Val Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly 290 295 300		
Val Ile Lys Cys Tyr Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu 305 310 315 320		
Glu Phe Glu His Phe Ser Val Phe Leu Glu Thr Phe His Val Thr Gln 325 330 335		
Tyr Phe Thr Val Arg Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys 340 345 350		
Ser Gln Cys Val Lys His Leu Gln Phe Thr Lys Trp Pro Asp His Gly		

B' af

355 360 365
 Thr Pro Ala Ser Ala Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg
 370 375 380
 Lys Ser His Ile Thr Gly Pro Leu Leu Val His Cys Ser Ala Gly Val
 385 390 395 400
 Gly Arg Thr Gly Val Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile
 405 410 415
 Glu Lys Asn Tyr Ser Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg
 420 425 430
 Lys Gln Arg Cys Gly Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys
 435 440 445
 Tyr Glu Ile Val Leu Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
 450 455 460

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15
 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30
 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys
 35 40 45
 Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp
 50 55 60
 Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu
 65 70 75 80
 Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95
 Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110
 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu

115 120 125
 Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140
 Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160
 Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175
 Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190
 Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205
 Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220
 His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240
 Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255
 Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr
 260 265 270
 Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285
 Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300
 Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320
 His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335
 Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350
 Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365
 Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380
 Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400
 Met Ile Gln Thr Lys
 405

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Phe Trp Gly Met Met Trp Glu Asn Asn Cys Asn Val Ile Ala Met
 1 5 10 15
 Ile Thr Arg Glu Ile Glu Gly Gly Val Ile Lys Cys Cys Ser Tyr Trp
 20 25 30
 Pro Val Ser Leu Lys Glu Pro Leu Glu Phe Lys His Phe His Val Leu
 35 40 45
 Leu Glu Asn Phe Gln Ile Thr Gln Tyr Phe Val Ile Arg Ile Phe Gln
 50 55 60
 Ile Val Lys Lys Ser Thr Gly Lys Ser His Ser Val Lys His Leu Gln
 65 70 75 80
 Phe Ile Lys Trp Pro Asp His Gly Thr Pro Ala Ser Val Asp Phe Phe
 85 90 95
 Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr Gly Pro Leu
 100 105 110
 Leu Val His Cys Thr Ala Gly Val Gly Arg
 115 120

B1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "Y" stands for C or T.
 The letter "V" stands for A, C or G.
 The letter "R" stands for A or G.
 The letter "N" stands for A, C, G

or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAYTTYTGGV RNATGRTNTG GGA

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "S" stands for C or G.
 The letter "Y" stands for C or T.
 The letter "N" stands for A, C, G
 or T.
 The letter "W" stands for A or T.
 The letter "R" stands for A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGCCSAYNC CNGCNSWRCA RTG

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 4 and 6 stand
 for an unspecified amino acid.
 "Xaa" in position 8 stands for
 either Glu or Asp.

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Phe Trp Xaa Met Xaa Trp Xaa

1

5

B1
enf

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 3 and 6 stand
 for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His Cys Xaa Ala Gly Xaa Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACCGTTTCA GTATTTTCTAGA TTGTGAAGAA GTCC

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACTTCTTC ACAATCTGAA ATACTCGAAC GGTG

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTTATGTG AGGAAGAGCC ACATTACAGG ACC

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACCGTTTCA GTATTTTACA TTGTGAAGAA GTCC

34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His Cys Ser Ala Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn
 20 25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr
 1 5 10 15

Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile
 20 25

B/W (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser Met Asp
 1 5 10 15

Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val
 20 25

110